



SEQUENCE LISTING

<110> KAO CORPORATION
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Takimura, Yasushi
Sato, Tsuyoshi

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<141> 2004-04-09

<150> 2003-106709

<151> 2003-04-10

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<170> PatentIn version 3.2

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115 120 125

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275 280 285

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Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr
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Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu
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Phe Thr Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu
 385 390 395 400

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Val Leu Gly Asn Gly Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn			
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Val Met Ala Pro Gly Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala
220 225 230 235

Pro Asp Ser Ser Phe Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met
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Gly Gly Thr Ser Met Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln
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270 275 280

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285 290 295

Tyr Pro Asn Gly Asn Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser
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Arg Asn Asn Val Glu Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr
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Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly		
		35					40					45					
aaa	ata	aca	gca	cta	tat	gca	ctg	ggt	cgg	acg	aat	aat	gcg	aat	gat		192
Lys	Ile	Thr	Ala	Leu	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Asn	Asp		
	50					55					60						
acg	aac	ggt	cat	ggt	acc	cat	gtg	gca	ggt	tcg	gta	tta	gga	aat	ggc		240
Thr	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Gly		
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gca	acg	aat	aaa	gga	atg	gca	cct	caa	gcg	aat	ctg	ggt	ttt	caa	tcc		288
Ala	Thr	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser		
			85					90						95			
atc	atg	gat	agc	agt	ggt	ggg	ctt	gga	ggc	ttg	cct	tcc	aat	ctg	caa		336
Ile	Met	Asp	Ser	Ser	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Leu	Gln		
			100					105					110				
acc	tta	ttc	agc	caa	gca	ttc	agt	gca	ggt	gcc	aga	att	cat	aca	aac		384
Thr	Leu	Phe	Ser	Gln	Ala	Phe	Ser	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn		
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Ser	Trp	Gly	Ala	Ala	Val	Asn	Gly	Ala	Tyr	Thr	Thr	Asp	Ser	Arg	Asn		
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Val	Asp	Asp	Tyr	Val	Arg	Lys	Asn	Asp	Met	Thr	Ile	Leu	Phe	Ala	Ala		
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ggg	aat	gaa	ggg	ccg	aac	ggc	ggt	acc	atc	agt	gca	cct	ggt	acg	gct		528
Gly	Asn	Glu	Gly	Pro	Asn	Gly	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala		
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aaa	aac	gcc	atc	act	gtc	ggc	gca	acc	gaa	aac	ctg	cgt	cca	agc	ttc		576
Lys	Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Leu	Arg	Pro	Ser	Phe		
			180					185					190				
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Gly	Ser	Tyr	Ala	Asp	Asn	Ile	Asn	His	Val	Ala	Gln	Phe	Ser	Ser	Arg		
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ggc	ccg	aca	aaa	gat	ggg	cga	atc	aag	cct	gat	gtc	atg	gcg	cca	ggg		672
Gly	Pro	Thr	Lys	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly		
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aca	tac	att	tta	tca	gca	aga	tct	tct	ctt	gca	ccc	gat	tcc	tcc	ttc		720
Thr	Tyr	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe		
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tgg	gcg	aat	cat	gac	agc	aaa	tat	gcc	tat	atg	ggt	gga	acg	tcc	atg		768
Trp	Ala	Asn	His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met		
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gca	aca	ccg	att	gtt	gcg	ggg	aat	gtt	gca	cag	ctc	cgt	gag	cat	ttt		816
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Leu Ile Ala Gly Ala Ala Asp Val Gly Leu Gly Tyr Pro Asn Gly Asn	290	295	300	
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Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr	305	310	315	320
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Val Asn Glu Ser Ser Ala Leu Ser Thr Ser Gln Lys Ala Thr Tyr Thr	325	330	335	
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Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser	340	345	350	
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Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu	355	360	365	
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Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp	370	375	380	
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 <213> Bacillus sp. KSM-kp9860

<400> 13

Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser
1 5 10 15

Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly
20 25 30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
50 55 60

Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly
65 70 75 80

Ala Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser
85 90 95

Ile Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln
100 105 110

Thr Leu Phe Ser Gln Ala Phe Ser Ala Gly Ala Arg Ile His Thr Asn
115 120 125

Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn
130 135 140

Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala
145 150 155 160

Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala
165 170 175

Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe
180 185 190

Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg
195 200 205

Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly
210 215 220

Thr Tyr Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe
225 230 235 240

Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met
245 250 255

Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe
260 265 270

Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala
 275 280 285

Leu Ile Ala Gly Ala Ala Asp Val Gly Leu Gly Tyr Pro Asn Gly Asn
 290 295 300

Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr
 305 310 315 320

Val Asn Glu Ser Ser Ala Leu Ser Thr Ser Gln Lys Ala Thr Tyr Thr
 325 330 335

Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser
 340 345 350

Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu
 355 360 365

Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp
 370 375 380

Phe Ser Ala Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu
 385 390 395 400

Asn Val Phe Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val
 405 410 415

Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile
 420 425 430

Val Asn

<210> 14
 <211> 1302
 <212> DNA
 <213> Bacillus sp. KSM-9865

<220>
 <221> CDS
 <222> (1)..(1302)
 <223> Protease 9865

<400> 14
 aat gat gtt gca cgt gga att gtc aaa gcg gat gtg gcg cag agc agc 48
 Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser
 1 5 10 15
 tac ggg ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg 96

Tyr	Gly	Leu	Tyr	Gly	Gln	Gly	Gln	Ile	Val	Ala	Val	Ala	Asp	Thr	Gly		
			20					25					30				
ctt	gat	aca	ggt	cgc	aat	gac	agt	tcg	atg	cat	gaa	gcc	ttc	cgg	ggg	144	
Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly		
		35					40					45					
aaa	att	act	gca	tta	tat	gca	ttg	gga	cgg	acg	aat	aat	gcc	aat	gat	192	
Lys	Ile	Thr	Ala	Leu	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Asn	Asp		
		50				55					60						
acg	aat	ggt	cat	ggt	acg	cat	gtg	gct	ggc	tcc	gta	tta	gga	aac	ggc	240	
Thr	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Gly		
		65			70				75						80		
tcc	act	aat	aaa	gga	atg	gcg	cct	cag	gcg	aat	cta	gtc	ttc	caa	tct	288	
Ser	Thr	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser		
			85					90					95				
atc	atg	gat	agc	ggt	ggg	gga	ctt	gga	gga	cta	cct	tcg	aat	ctg	caa	336	
Ile	Met	Asp	Ser	Gly	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Leu	Gln		
			100					105					110				
acc	tta	ttc	agc	caa	gca	tac	agt	gct	ggg	gcc	aga	att	cat	aca	aac	384	
Thr	Leu	Phe	Ser	Gln	Ala	Tyr	Ser	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn		
		115					120					125					
tcc	tgg	gga	gca	gca	gtg	aat	ggg	gct	tac	aca	aca	gat	tcc	aga	aat	432	
Ser	Trp	Gly	Ala	Ala	Val	Asn	Gly	Ala	Tyr	Thr	Thr	Asp	Ser	Arg	Asn		
		130				135						140					
gtg	gat	gac	tat	gtg	cgc	aaa	aat	gat	atg	acg	atc	ctt	ttc	gct	gcc	480	
Val	Asp	Asp	Tyr	Val	Arg	Lys	Asn	Asp	Met	Thr	Ile	Leu	Phe	Ala	Ala		
					150					155					160		
ggg	aat	gaa	gga	ccg	aac	ggc	gga	acc	atc	agt	gca	cca	ggc	aca	gct	528	
Gly	Asn	Glu	Gly	Pro	Asn	Gly	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala		
				165					170					175			
aaa	aat	gca	ata	aca	gtc	gga	gct	acg	gaa	aac	ctc	cgc	cca	agc	ttc	576	
Lys	Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Leu	Arg	Pro	Ser	Phe		
			180					185					190				
ggg	tct	tat	gcg	gac	aat	atc	aac	cat	gtg	gca	cag	ttc	tct	tca	cgt	624	
Gly	Ser	Tyr	Ala	Asp	Asn	Ile	Asn	His	Val	Ala	Gln	Phe	Ser	Ser	Arg		
		195				200						205					
gga	ccg	aca	aag	gat	gga	cgg	atc	aaa	ccg	gat	gtc	atg	gca	ccg	gga	672	
Gly	Pro	Thr	Lys	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly		
		210				215					220						
acg	ttc	ata	cta	tca	gca	aga	tct	tct	ctt	gca	ccg	gat	tcc	tcc	ttc	720	
Thr	Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe		
					230					235					240		
tgg	gcg	aac	cat	gac	agt	aaa	tat	gca	tac	atg	ggt	gga	acg	tcc	atg	768	
Trp	Ala	Asn	His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met		
				245					250					255			
gct	aca	ccg	atc	gtt	gct	gga	aac	gtg	gca	cag	ctt	cgt	gag	cat	ttt	816	
Ala	Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe		

	260	265	270	
gtg aaa aac aga ggc atc aca cca aag cct tct cta tta aaa gcg gca				864
Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala				
	275	280	285	
ctg att gcc ggt gca gca gac atc ggc ctt ggc tac ccg aac ggt aac				912
Leu Ile Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn				
	290	295	300	
caa gga tgg gga cga gtg aca ttg gat aaa tcc cta aac gtt gcc tat				960
Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr				
	305	310	315	320
gtg aac gag tcc agt tct cta tcc acc agc caa aaa gcg acg tac tcg				1008
Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser				
	325	330	335	
ttt act gct act gcc ggc aag cct ttg aag atc tcc ctg gta tgg tct				1056
Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser				
	340	345	350	
gat gcc cct gcg agc aca act gct tcc gta acg ctt gtc aat gac ctg				1104
Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu				
	355	360	365	
gac ctt gtc att acc gct cca aat ggc aca caa tat gtt gga aat gac				1152
Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp				
	370	375	380	
ttt act tcg cca tac aat aat aac tgg gat ggc cgc aat aac gta gaa				1200
Phe Thr Ser Pro Tyr Asn Asn Asn Trp Asp Gly Arg Asn Asn Val Glu				
	385	390	395	400
aat gta ttt att aat gcg cca caa agc ggg acg tat aca att gag gta				1248
Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val				
	405	410	415	
cag gct tat aac gta ccg gtt gga cca cag acc ttc tcg ttg gca att				1296
Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile				
	420	425	430	
gtg aac				1302
Val Asn				

<210> 15
 <211> 434
 <212> PRT
 <213> Bacillus sp. KSM-9865

<400> 15

Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser			
1	5	10	15

Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly			
20	25	30	

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
50 55 60

Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly
65 70 75 80

Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser
85 90 95

Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln
100 105 110

Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn
115 120 125

Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn
130 135 140

Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala
145 150 155 160

Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala
165 170 175

Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe
180 185 190

Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg
195 200 205

Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly
210 215 220

Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe
225 230 235 240

Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met
245 250 255

Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe
260 265 270

Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala
 275 280 285

Leu Ile Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn
 290 295 300

Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr
 305 310 315 320

Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser
 325 330 335

Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser
 340 345 350

Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu
 355 360 365

Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp
 370 375 380

Phe Thr Ser Pro Tyr Asn Asn Asn Trp Asp Gly Arg Asn Asn Val Glu
 385 390 395 400

Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val
 405 410 415

Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile
 420 425 430

Val Asn

<210> 16
 <211> 1299
 <212> DNA
 <213> Bacillus sp. D-6

<220>
 <221> CDS
 <222> (1)..(1299)
 <223> Protease E-1

<400> 16
 aat gat gta gca aga gga ata gta aaa gca gac gtt gca caa aac aat 48
 Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn
 1 5 10 15
 tac gga cta tat gga caa ggt caa gta gtt gca gta gcg gat acg ggt 96

Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly	
20 25 30	
tta gat aca ggt cgt aac gat agt tct atg cat gaa gca ttc cgt ggg	144
Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly	
35 40 45	
aaa att aca gct ctt tac gcg tta gga aga act aac aat gca aat gat	192
Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp	
50 55 60	
ccg aat ggg cat ggt acg cat gta gct ggt tct gtg ctt ggt aat gct	240
Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala	
65 70 75 80	
tta aat aaa gga atg gct ccg caa gct aac tta gtc ttc caa tct att	288
Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile	
85 90 95	
atg gat agc agc gga gga tta gga gga tta cca tcg aat tta aat acg	336
Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr	
100 105 110	
tta ttt agt caa gct tgg aat gct ggc gct aga att cat act aac tct	384
Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser	
115 120 125	
tgg ggg gcc cca gta aat gga gcg tac act gct aac tcg aga caa gtg	432
Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val	
130 135 140	
gat gag tat gtt cga aac aat gat atg acg gta ctt ttt gca gct gga	480
Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly	
145 150 155 160	
aat gaa gga cct aac tct gga aca att agc gct cca ggg aca gcg aaa	528
Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys	
165 170 175	
aat gcc att acg gtc ggc gca acg gaa aac tac cga cca agt ttt ggt	576
Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly	
180 185 190	
tca att gca gat aac cct aat cat atc gca caa ttt tca tcg aga gga	624
Ser Ile Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly	
195 200 205	
gct acg aga gat gga cga att aaa cca gac gta aca gct cct gga aca	672
Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr	
210 215 220	
ttt ata tta tca gca cgc tct tct tta gca cca gac tct tcg ttt tgg	720
Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp	
225 230 235 240	
gcg aat tat aac agt aag tat gcg tat atg ggc ggt acc tct atg gcg	768
Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala	
245 250 255	
aca cct ata gtt gcg ggg aat gtc gcg caa tta cgc gag cat ttt ata	816
Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile	

260	265	270	
aaa aat aga gga att aca cct	aaa cct tcc tta ata	aaa gct gca ctt	864
Lys Asn Arg Gly Ile Thr Pro	Lys Pro Ser Leu Ile Lys	Ala Ala Leu	
275	280	285	
atc gct ggg gct act gat gtt ggt tta gga tat cca agt ggt gac caa			912
Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Ser Gly Asp Gln			
290	295	300	
ggc tgg ggg cgt gtt act tta gat aaa tcg tta aat gta gcg tat gtc			960
Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val			
305	310	315	320
aat gaa gca act gca tta aca aca gga caa aaa gca acg tat tcg ttc			1008
Asn Glu Ala Thr Ala Leu Thr Thr Gly Gln Lys Ala Thr Tyr Ser Phe			
325	330	335	
caa acg caa gcg ggt aaa cca tta aaa atc tcg tta gta tgg aca gat			1056
Gln Thr Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp			
340	345	350	
gca cct gga agt aca aca gca tct tat aca cta gtt aat gat tta gat			1104
Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp			
355	360	365	
cta gtt att act gct ccg aat gga caa aaa tat gta ggt aat gat ttt			1152
Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe			
370	375	380	
agt tat cct tat gat aat aat tgg gat ggt cgc aac aat gtt gag aac			1200
Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn			
385	390	395	400
gta ttt ata aac gct ccg caa tct gga acg tat aca att gag gtt caa			1248
Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln			
405	410	415	
gcg tat aac gtt cca tct gga cca cag cgt ttc tca cta gct atc gta			1296
Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val			
420	425	430	
cat			1299
His			

<210> 17
 <211> 433
 <212> PRT
 <213> Bacillus sp. D-6

<400> 17

Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn
1 5 10 15

Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly
20 25 30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
50 55 60

Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala
65 70 75 80

Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile
85 90 95

Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr
100 105 110

Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser
115 120 125

Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val
130 135 140

Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly
145 150 155 160

Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys
165 170 175

Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly
180 185 190

Ser Ile Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly
195 200 205

Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr
210 215 220

Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp
225 230 235 240

Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala
245 250 255

Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile
260 265 270

Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu
 275 280 285

Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Ser Gly Asp Gln
 290 295 300

Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val
 305 310 315 320

Asn Glu Ala Thr Ala Leu Thr Thr Gly Gln Lys Ala Thr Tyr Ser Phe
 325 330 335

Gln Thr Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp
 340 345 350

Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp
 355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe
 370 375 380

Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn
 385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln
 405 410 415

Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val
 420 425 430

His

<210> 18
 <211> 1299
 <212> DNA
 <213> Bacillus sp. Y

<220>
 <221> CDS
 <222> (1)..(1299)
 <223> Gene name Ya,
 Protease Ya

<400> 18
 aat gat gta gca aga ggg ata gta aaa gct gat gtt gca caa aac aat
 Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn
 1 5 10 15

tac gga tta tat gga caa ggt caa gta gtt gca gta gcg gac aca ggc Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly 20 25 30	96
tta gat aca ggt cgt aac gat agt tct atg cat gaa gca ttc cgc ggg Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly 35 40 45	144
aaa atc aca gct ctt tac gcg tta gga aga act aat aat gcg agt gat Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Ser Asp 50 55 60	192
ccg aat ggg cat ggc aca cat gta gca ggt tct gta ctt ggt aat gct Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala 65 70 75 80	240
tta aat aaa gga atg gct ccg caa gct aac tta gtc ttc caa tct att Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile 85 90 95	288
atg gat agc agc gga gga tta ggt ggc tta cca tcg aac tta aat acg Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr 100 105 110	336
tta ttt agt caa gct tgg aat gct gga gca aga att cat act aac tct Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser 115 120 125	384
tgg gga gcc cca gta aat gga gcg tac act gct aac tcg aga caa gtg Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val 130 135 140	432
gat gaa tat gtt cga aat aat gat atg acg gta ctt ttt gca gct ggt Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly 145 150 155 160	480
aat gaa ggt cct aat tca gga aca att agt gct cca ggt aca gcg aaa Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys 165 170 175	528
aat gct att acg gtc ggc gca acg gaa aac tat cgc cca agc ttc ggt Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly 180 185 190	576
tcg ata gca gat aac cca aat cat att gca caa ttt tca tcg aga gga Ser Ile Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly 195 200 205	624
gct acg agg gat gga cga att aag cct gac gta aca gct cct gga aca Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr 210 215 220	672
ttt att tta tca gca cgt tct tcc tta gct cca gac tct tcg ttt tgg Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp 225 230 235 240	720
gcg aat tat aac agt aaa tac gcg tat atg ggc ggt acc tcc atg gcg Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala 245 250 255	768
aca cct att gtt gca ggg aat gtc gcg caa tta cgt gag cat ttt ata	816

Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	Ile		
			260					265					270				
aaa	aat	aga	ggt	att	act	cct	aag	cct	tct	tta	ata	aaa	gct	gca	ctt	864	
Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Ile	Lys	Ala	Ala	Leu		
		275					280					285					
atc	gct	ggt	gct	act	gat	gtt	ggt	tta	gga	tat	cct	aat	ggt	gac	caa	912	
Ile	Ala	Gly	Ala	Thr	Asp	Val	Gly	Leu	Gly	Tyr	Pro	Asn	Gly	Asp	Gln		
	290					295					300						
ggc	tgg	ggg	cgt	gtt	act	cta	aat	aaa	tcg	tta	aat	gta	gcg	tat	gtc	960	
Gly	Trp	Gly	Arg	Val	Thr	Leu	Asn	Lys	Ser	Leu	Asn	Val	Ala	Tyr	Val		
305				310					315						320		
aat	gaa	gca	act	gca	tta	gcc	aca	gga	caa	aaa	gca	acg	tat	tcg	ttc	1008	
Asn	Glu	Ala	Thr	Ala	Leu	Ala	Thr	Gly	Gln	Lys	Ala	Thr	Tyr	Ser	Phe		
			325					330						335			
caa	gca	caa	gcg	ggt	aaa	cct	tta	aaa	atc	tcg	tta	gta	tgg	aca	gat	1056	
Gln	Ala	Gln	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Thr	Asp		
		340					345						350				
gct	cct	gga	agt	aca	act	gca	tct	tat	aca	cta	gtt	aat	gat	tta	gat	1104	
Ala	Pro	Gly	Ser	Thr	Thr	Ala	Ser	Tyr	Thr	Leu	Val	Asn	Asp	Leu	Asp		
	355					360						365					
cta	gtt	att	act	gct	ccg	aat	gga	caa	aaa	tat	gta	gga	aat	gat	ttt	1152	
Leu	Val	Ile	Thr	Ala	Pro	Asn	Gly	Gln	Lys	Tyr	Val	Gly	Asn	Asp	Phe		
	370					375					380						
agt	tat	cct	tat	gat	aat	aac	tgg	gat	ggt	cgc	aac	aat	gtt	gag	aac	1200	
Ser	Tyr	Pro	Tyr	Asp	Asn	Asn	Trp	Asp	Gly	Arg	Asn	Asn	Val	Glu	Asn		
385				390					395					400			
gta	ttt	ata	aac	gct	ccg	caa	tct	gga	acg	tat	ata	att	gag	gtt	caa	1248	
Val	Phe	Ile	Asn	Ala	Pro	Gln	Ser	Gly	Thr	Tyr	Ile	Ile	Glu	Val	Gln		
			405					410					415				
gcg	tat	aat	gta	cca	tct	ggc	cca	cag	cgt	ttc	tca	cta	gct	atc	gta	1296	
Ala	Tyr	Asn	Val	Pro	Ser	Gly	Pro	Gln	Arg	Phe	Ser	Leu	Ala	Ile	Val		
		420					425					430					
cat																1299	
His																	

<210> 19
 <211> 433
 <212> PRT
 <213> Bacillus sp. Y

<400> 19

Asn	Asp	Val	Ala	Arg	Gly	Ile	Val	Lys	Ala	Asp	Val	Ala	Gln	Asn	Asn
1			5					10					15		

Tyr	Gly	Leu	Tyr	Gly	Gln	Gly	Gln	Val	Val	Ala	Val	Ala	Asp	Thr	Gly
		20					25						30		

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Ser Asp
50 55 60

Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala
65 70 75 80

Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile
85 90 95

Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr
100 105 110

Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser
115 120 125

Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val
130 135 140

Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly
145 150 155 160

Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys
165 170 175

Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly
180 185 190

Ser Ile Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly
195 200 205

Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr
210 215 220

Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp
225 230 235 240

Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala
245 250 255

Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile
260 265 270

Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu
 275 280 285

Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Asn Gly Asp Gln
 290 295 300

Gly Trp Gly Arg Val Thr Leu Asn Lys Ser Leu Asn Val Ala Tyr Val
 305 310 315 320

Asn Glu Ala Thr Ala Leu Ala Thr Gly Gln Lys Ala Thr Tyr Ser Phe
 325 330 335

Gln Ala Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp
 340 345 350

Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp
 355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe
 370 375 380

Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn
 385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Ile Ile Glu Val Gln
 405 410 415

Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val
 420 425 430

His

<210> 20
 <211> 1299
 <212> DNA
 <213> Bacillus SD521

<220>
 <221> CDS
 <222> (1)..(1299)
 <223> Gene name SD-521, protease SD521

<400> 20
 aat gat gta gca aga gga ata gta aaa gca gac gtt gca caa aac aat
 Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn
 1 5 10 15

tac gga cta tat gga caa ggt caa gta gtt gca gta gcg gat acg ggt Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly 20 25 30	96
tta gat aca ggt cgt aac gat agt tct atg cat gaa gca ttc cgt ggg Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly 35 40 45	144
aaa att aca gct ctt tac gcg tta gga aga act aac aat gca aat gat Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp 50 55 60	192
ccg aat ggg cat ggt acg cat gta gca ggt tct gta ctt ggt aat gct Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala 65 70 75 80	240
tta aat aaa gga atg gct ccg caa gct aac tta gtc ttc caa tct att Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile 85 90 95	288
atg gat agc agc gga gga tta ggt gga tta cca tcg aat ttg aat acg Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr 100 105 110	336
tta ttt agt caa gct tgg aat gct ggg gct aga att cat act aac tct Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser 115 120 125	384
tgg ggt gct cca gta aat gga gcg tac act gct aac tcg aga caa gtg Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val 130 135 140	432
gat gag tat gtt cga aat aat gat atg acg gta ctt ttt gca gca ggt Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly 145 150 155 160	480
aat gaa ggt cct aat tca gga aca att agt gct cca ggc aca gcg aaa Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys 165 170 175	528
aat gcc att acg gtc ggc gca acg gaa aac tat cgc ccg agc ttc ggt Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly 180 185 190	576
tca tta gca gat aac cca aat cat atc gca caa ttt tca tca aga gga Ser Leu Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly 195 200 205	624
gct acg aga gat gga cga att aaa cca gac gta aca gct cct gga aca Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr 210 215 220	672
ttt att tta tca gca cgt tct tcc tta gcc cca gac tct tcg ttt tgg Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp 225 230 235 240	720
gcg aat tat aac agt aag tat gcg tac atg ggc ggt acc tct atg gcg Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala 245 250 255	768
aca cct ata gtt gcg ggg aat gtc gcg caa tta cgc gag cat ttt ata	816

Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	Ile		
			260					265					270				
aaa	aat	aga	gga	att	aca	cct	aaa	cct	tcc	tta	ata	aaa	gct	gca	ctt		864
Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Ile	Lys	Ala	Ala	Leu		
			275				280					285					
atc	gct	ggg	gct	act	gat	gtt	ggg	tta	gga	tat	cca	agt	ggg	gac	caa		912
Ile	Ala	Gly	Ala	Thr	Asp	Val	Gly	Leu	Gly	Tyr	Pro	Ser	Gly	Asp	Gln		
			290			295				300							
ggc	tgg	ggg	cgt	gtt	act	cta	gat	aaa	tcg	tta	aat	gta	gcg	tat	gtc		960
Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	Val		
					310					315					320		
aat	gaa	gca	act	gca	tta	gca	aca	gga	caa	aaa	gca	acg	tat	tcg	ttc		1008
Asn	Glu	Ala	Thr	Ala	Leu	Ala	Thr	Gly	Gln	Lys	Ala	Thr	Tyr	Ser	Phe		
				325					330					335			
caa	gca	caa	gcg	ggg	aaa	cct	tta	aaa	atc	tcg	tta	gta	tgg	aca	gat		1056
Gln	Ala	Gln	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Thr	Asp		
			340					345					350				
gca	cct	gga	agt	aca	act	gca	tct	tat	aca	cta	gtt	aat	gat	tta	gat		1104
Ala	Pro	Gly	Ser	Thr	Thr	Ala	Ser	Tyr	Thr	Leu	Val	Asn	Asp	Leu	Asp		
			355				360					365					
cta	gtt	att	act	gct	ccg	aat	gga	caa	aaa	tat	gta	gga	aat	gat	ttt		1152
Leu	Val	Ile	Thr	Ala	Pro	Asn	Gly	Gln	Lys	Tyr	Val	Gly	Asn	Asp	Phe		
			370			375					380						
agt	tat	cct	tat	gat	aat	aac	tgg	gat	ggg	cgc	aac	aat	gtt	gag	aac		1200
Ser	Tyr	Pro	Tyr	Asp	Asn	Asn	Trp	Asp	Gly	Arg	Asn	Asn	Val	Glu	Asn		
					390					395					400		
gta	ttt	ata	aac	gct	ccg	caa	tct	gga	acg	tat	aca	att	gag	gtt	caa		1248
Val	Phe	Ile	Asn	Ala	Pro	Gln	Ser	Gly	Thr	Tyr	Thr	Ile	Glu	Val	Gln		
				405				410						415			
gcg	tat	aat	gta	cca	tct	ggc	cca	cag	cgt	ttc	tca	cta	gct	atc	gta		1296
Ala	Tyr	Asn	Val	Pro	Ser	Gly	Pro	Gln	Arg	Phe	Ser	Leu	Ala	Ile	Val		
			420					425					430				
cat																	1299
His																	

<210> 21
 <211> 433
 <212> PRT
 <213> Bacillus SD521

<400> 21

Asn	Asp	Val	Ala	Arg	Gly	Ile	Val	Lys	Ala	Asp	Val	Ala	Gln	Asn	Asn
1				5				10					15		

Tyr	Gly	Leu	Tyr	Gly	Gln	Gly	Gln	Val	Val	Ala	Val	Ala	Asp	Thr	Gly
			20					25					30		

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
50 55 60

Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala
65 70 75 80

Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile
85 90 95

Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr
100 105 110

Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser
115 120 125

Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val
130 135 140

Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly
145 150 155 160

Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys
165 170 175

Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly
180 185 190

Ser Leu Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly
195 200 205

Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr
210 215 220

Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp
225 230 235 240

Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala
245 250 255

Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile
260 265 270

Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu
 275 280 285

Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Ser Gly Asp Gln
 290 295 300

Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val
 305 310 315 320

Asn Glu Ala Thr Ala Leu Ala Thr Gly Gln Lys Ala Thr Tyr Ser Phe
 325 330 335

Gln Ala Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp
 340 345 350

Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp
 355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe
 370 375 380

Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn
 385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln
 405 410 415

Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val
 420 425 430

His

<210> 22
 <211> 1302
 <212> DNA
 <213> Bacillus NCIB12289

<220>
 <221> CDS
 <222> (1)..(1302)
 <223> Gene name A1, protease A1

<400> 22
 aac gat gtt gcc aga ggc att gta aaa gcc gat gtt gcc cag agc agc
 Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser
 1 5 10 15

tat ggt tta tat ggg caa ggg caa gtg gtt gca gta gcg gat acc gga Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly 20 25 30	96
ctg gat aca ggg cgt aat gac agc tcg atg cat gaa gcg ttc cga gga Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly 35 40 45	144
aag att acc gcg ata tat gcc ctt gga aga aca aac aac gcc aat gat Lys Ile Thr Ala Ile Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp 50 55 60	192
cca aac gga cac ggg acg cat gtt gcc gga tct gtt tta gga aac ggt Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly 65 70 75 80	240
act tcg aat aaa ggg atg gct cca caa gct aac tta gtt ttc caa tct Thr Ser Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser 85 90 95	288
gtt atg gac agc aat ggc gga ctt ggc gga ctg cct tcc aat gta agt Val Met Asp Ser Asn Gly Gly Leu Gly Gly Leu Pro Ser Asn Val Ser 100 105 110	336
aca tta ttc agc cag gca tat agt gcc ggt gcc aga atc cat acg aac Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn 115 120 125	384
tca tgg gga gcg cct gta aac gga gcg tac act act gat tcc aga aac Ser Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn 130 135 140	432
gta gac gat tat gtt cgt aaa aat gat atg gcg gtt ctt ttt gca gcg Val Asp Asp Tyr Val Arg Lys Asn Asp Met Ala Val Leu Phe Ala Ala 145 150 155 160	480
ggt aac gaa ggg ccg aat ggc ggc aca atc agt gct cct ggt acc gcg Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala 165 170 175	528
aag aat gct atc aca gta ggg gca aca gaa aac ctg cgc cca agc ttt Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe 180 185 190	576
gga tct tat gct gac aac atc aat cat gta gca cag ttt tcc tcc cgc Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg 195 200 205	624
gga cct aca aag gat gga cgt atc aaa ccg gac gta atg gca cca gga Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly 210 215 220	672
aca ttt att tta tcg gca aga tct tct ttg gct ccg gac tcc tca ttc Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe 225 230 235 240	720
tgg gca aac cat gac agc aaa tat gct tat atg ggt gga aca tcc atg Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met 245 250 255	768
gcg aca ccg att gta gct ggt aac gtt gca cag tta cgt gaa cat ttc	816

Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe	
260 265 270	
atc aaa aac aga gga atc act cct aaa cca tcc ttg ctg aaa gca gct	864
Ile Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala	
275 280 285	
ctt att gcc gga gca act gat atc ggt ctt ggc tat ccg agt gga aac	912
Leu Ile Ala Gly Ala Thr Asp Ile Gly Leu Gly Tyr Pro Ser Gly Asn	
290 295 300	
caa gga tgg gga aga gta aca ttg gac aag tca ctt aat gta gct ttc	960
Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Phe	
305 310 315 320	
gta aat gaa aca agc tct tta tct act aac caa aag gct acg tat tca	1008
Val Asn Glu Thr Ser Ser Leu Ser Thr Asn Gln Lys Ala Thr Tyr Ser	
325 330 335	
ttt act gca caa tca ggc aaa cct ttg aag att tca ttg gtt tgg tct	1056
Phe Thr Ala Gln Ser Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser	
340 345 350	
gat gca ccg gca agt act tcc gca tcg gtt aca ttg gtg aat gat ctg	1104
Asp Ala Pro Ala Ser Thr Ser Ala Ser Val Thr Leu Val Asn Asp Leu	
355 360 365	
gat ctg gtg att aca gct cca aat gga aca aag tat gtt gga aac gac	1152
Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Lys Tyr Val Gly Asn Asp	
370 375 380	
ttt act gct ccc tat gat aat aac tgg gat gga cgt aac aat gta gag	1200
Phe Thr Ala Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu	
385 390 395 400	
aac gtg ttt atc aat gct ccg caa agc gga acg tat aca gtt gag gta	1248
Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Val Glu Val	
405 410 415	
cag gct tac aat gtt cca caa ggg ccg cag gcg ttt tct ttg gct att	1296
Gln Ala Tyr Asn Val Pro Gln Gly Pro Gln Ala Phe Ser Leu Ala Ile	
420 425 430	
gtg aac	1302
Val Asn	

<210> 23
 <211> 434
 <212> PRT
 <213> Bacillus NCIB12289

<400> 23

Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser
1 5 10 15

Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly
20 25 30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
35 40 45

Lys Ile Thr Ala Ile Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
50 55 60

Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly
65 70 75 80

Thr Ser Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser
85 90 95

Val Met Asp Ser Asn Gly Gly Leu Gly Gly Leu Pro Ser Asn Val Ser
100 105 110

Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn
115 120 125

Ser Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn
130 135 140

Val Asp Asp Tyr Val Arg Lys Asn Asp Met Ala Val Leu Phe Ala Ala
145 150 155 160

Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala
165 170 175

Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe
180 185 190

Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg
195 200 205

Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly
210 215 220

Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe
225 230 235 240

Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met
245 250 255

Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe
260 265 270

Ile Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala
 275 280 285

Leu Ile Ala Gly Ala Thr Asp Ile Gly Leu Gly Tyr Pro Ser Gly Asn
 290 295 300

Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Phe
 305 310 315 320

Val Asn Glu Thr Ser Ser Leu Ser Thr Asn Gln Lys Ala Thr Tyr Ser
 325 330 335

Phe Thr Ala Gln Ser Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser
 340 345 350

Asp Ala Pro Ala Ser Thr Ser Ala Ser Val Thr Leu Val Asn Asp Leu
 355 360 365

Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Lys Tyr Val Gly Asn Asp
 370 375 380

Phe Thr Ala Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu
 385 390 395 400

Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Val Glu Val
 405 410 415

Gln Ala Tyr Asn Val Pro Gln Gly Pro Gln Ala Phe Ser Leu Ala Ile
 420 425 430

Val Asn

<210> 24
 <211> 433
 <212> PRT
 <213> Bacillus NCIB12513

<400> 24

Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn
 1 5 10 15

Phe Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly
 20 25 30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly

25

40

45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
50 55 60

Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala
65 70 75 80

Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile
85 90 95

Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ala Asn Leu Gln Thr
100 105 110

Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser
115 120 125

Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val
130 135 140

Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly
145 150 155 160

Asn Glu Gly Pro Gly Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys
165 170 175

Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly
180 185 190

Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly
195 200 205

Pro Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr
210 215 220

Tyr Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp
225 230 235 240

Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala
245 250 255

Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val
260 265 270

Lys Asn Arg Gly Val Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu
275 280 285

Ile Ala Gly Ala Ala Asp Val Gly Leu Gly Phe Pro Asn Gly Asn Gln
290 295 300

Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Phe Val
305 310 315 320

Asn Glu Thr Ser Pro Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe
325 330 335

Thr Ala Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp
340 345 350

Ala Pro Gly Ser Thr Thr Ala Ser Leu Thr Leu Val Asn Asp Leu Asp
355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Thr Lys Tyr Val Gly Asn Asp Phe
370 375 380

Thr Ala Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn
385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Val Glu Val Gln
405 410 415

Ala Tyr Asn Val Pro Val Ser Pro Gln Thr Phe Ser Leu Ala Ile Val
420 425 430

His